DB Name	Query	Hit Count	Set Name
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	fusobacterium and shuttle vector	2	L8
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	fusobacterium same shuttle vector	0	L7
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	fusobacterium and (repa or repA)	2	L6
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	fusobacterium same plasmid	2	L5
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	fusobacterium same pfn1	0	L4
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	fusobacterium same (ori or origin of replication or replication origin)	1	L3
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	fusobacterium and (ori or origin of replication or replication origin)	23	L2
USPT,PGPB,JPAB,EPAB,DWPI,TDBD	fusobacterium and iteron	0	L1

Attachment to paper # 5
FOAM

WEST

Help | Logout | Interrupt

Main Menu | Search Form | Posting Counts | Show S Numbers | Edit S Numbers | Preferences

Search Results -

Term	Documents
FUSOBACTERIUM.DWPI,TDBD,EPAB,JPAB,USPT,PGPB.	753
FUSOBACTERIUMS	0
FUSOBACTERIA.DWPI,TDBD,EPAB,JPAB,USPT,PGPB.	37
FUSOBACTERIAS	0
SHUTTLE.DWPI,TDBD,EPAB,JPAB,USPT,PGPB.	31867
SHUTTLES.DWPI,TDBD,EPAB,JPAB,USPT,PGPB.	3618
VECTOR.DWPI,TDBD,EPAB,JPAB,USPT,PGPB.	170967
VECTORS.DWPI,TDBD,EPAB,JPAB,USPT,PGPB.	81110
(FUSOBACTERIUM AND (SHUTTLE ADJ VECTOR)).USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	2

Database: US Patents Full-Text Database; US Pre-Grant Publication Full-Text Database; JPO Abstracts Database; EPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Refine Search: fusobacterium and shuttle vector

Clear

Search History

Today's Date: 8/24/2001

```
### Status: Path 1 of [Dialog Information Services via Modem]

### Status: Initializing TCP/IP using (UseTelnetProto 1 ServiceID pto-dialog)
Trying 3106900061...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 01.08.22D

Last logoff:  24aug01 09:28:23
Logon file001 24aug01 17:33:38
KWIC is set to 50.
HILIGHT set on as '*'
 * * *                                    * * *

File   1:ERIC  1966-2001/Aug 17
       (c) format only 2001 The Dialog Corporation

      Set  Items  Description
      ---  -----  -----------
?b 5, 434, 155
       24aug01 17:33:42 User259980 Session D148.1
            $0.25    0.072 DialUnits File1
     $0.25  Estimated cost File1
     $0.25  Estimated cost this search
     $0.25  Estimated total session cost   0.072 DialUnits


SYSTEM:OS  - DIALOG OneSearch
  File   5:Biosis Previews(R)  1969-2001/Aug W3
         (c) 2001 BIOSIS
  File 434:SciSearch(R) Cited Ref Sci  1974-1989/Dec
         (c) 1998 Inst for Sci Info
  File 155:MEDLINE(R)  1966-2001/Sep W3

      Set  Items  Description
      ---  -----  -----------
?s fusobacterium and iteron
            6050  FUSOBACTERIUM
             116  ITERON
      S1       0  FUSOBACTERIUM AND ITERON
?s fusobacterium(s)(ori or origin)
            6050  FUSOBACTERIUM
            1889  ORI
          292582  ORIGIN
      S2      73  FUSOBACTERIUM(S)(ORI OR ORIGIN)
?rd
...examined 50 records  (50)
...completed examining records
      S3      53  RD (unique items)
?s s3 and pnf1
              53  S3
               4  PNF1
      S4       0  S3 AND PNF1
?s s3 and plasmid
              53  S3
          122510  PLASMID
      S5       0  S3 AND PLASMID
?s s3 and repa
              53  S3
             764  REPA
```

```
      S6        0  S3 AND REPA
? s s3 and rep
              53  S3
            3654  REP
      S7        0  S3 AND REP
?s fusobacterium and electropor?
            6050  FUSOBACTERIUM
            7344  ELECTROPOR?
      S8        4  FUSOBACTERIUM AND ELECTROPOR?
?rd
...completed examining records
      S9        4  RD (unique items)
?t/9/all

 9/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

12030651   BIOSIS NO.: 199900311170
Transformation of *Fusobacterium* nucleatum by *electroporation*.
AUTHOR: Haake S Kinder(a); Yoder S C(a)
AUTHOR ADDRESS: (a)School of Dentistry, UCLA, Los Angeles, CA**USA
JOURNAL: Abstracts of the General Meeting of the American Society for
Microbiology  99p331 1999
CONFERENCE/MEETING: 99th General Meeting of the American Society for
Microbiology  Chicago, Illinois, USA  May 30-June 3, 1999
SPONSOR: American Society for Microbiology
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
DESCRIPTORS:
  MAJOR CONCEPTS: Methods and Techniques; Molecular Genetics (Biochemistry
    and Molecular Biophysics)
  BIOSYSTEMATIC NAMES: Bacteroidaceae--Anaerobic Gram-Negative Rods,
    Eubacteria, Bacteria, Microorganisms; Enterobacteriaceae--Facultatively
    Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms
  ORGANISMS: E. coli (Escherichia coli) (Enterobacteriaceae);
    *Fusobacterium* nucleatum (Bacteroidaceae)
  BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria;
    Microorganisms
  CHEMICALS & BIOCHEMICALS:   pHS17--shuttle plasmid;  DNA--transfer
  METHODS & EQUIPMENT: *electroporation*--DNA transfer method
  MISCELLANEOUS TERMS:   Meeting Abstract; Meeting Poster
CONCEPT CODES:
  31500   Genetics of Bacteria and Viruses
  10050   Biochemical Methods-General
  10060   Biochemical Studies-General
  32000   Microbiological Apparatus, Methods and Media
  31000   Physiology and Biochemistry of Bacteria
  00520   General Biology-Symposia, Transactions and Proceedings of
             Conferences, Congresses, Review Annuals
BIOSYSTEMATIC CODES:
  06702   Enterobacteriaceae (1992- )
  06901   Bacteroidaceae (1992- )


 9/9/2     (Item 2 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
(c) 2001 BIOSIS. All rts. reserv.

11623650   BIOSIS NO.: 199800405846
Dentilism activity affects the organization of the outer sheath of
 Treponema denticola.
AUTHOR: Ishihara Kazuyuki(a); Kuramitsu Howard K; Miura Tadashi; Okuda
  Katsuji
AUTHOR ADDRESS: (a)Dep. Microbiol., Oral Health Sci. Cent., Tokyo Dent.
  Coll., 1-2-2 Masago, Mihama-ku, Chiba 261-8**Japan
JOURNAL: Journal of Bacteriology  180 (15):p3837-3844 Aug., 1998
ISSN: 0021-9193
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
```

LANGUAGE: English

ABSTRACT: Prolyl-phenylalanine-specific serine protease (dentilisin) is a major extracellular protease produced by Treponema denticola. The gene, prtP, coding for the protease was recently cloned and sequenced (K. Ishihara, T. Miura, H. K. Kuramitsu, and K. Okuda, Infect. Immun. 64:5178-5186,1996). In order to determine the role of this protease in the physiology and virulence of T. denticola, a dentilisin-deficient mutant, K1, was constructed following *electroporation* with a prtP-inactivated DNA fragment. No chymotrypsin-like protease activity was detected in the dentilisin-deficient mutant. In addition, the high-molecular-mass oligomeric protein characteristic of the outer sheath of the organism decreased in the mutant. Furthermore, the hydrophobicity of the mutant was decreased, and coaggregation of the mutant with *Fusobacterium* nucleatum was enhanced compared to that of the wild-type organism. The results obtained with a mouse abscess model system indicated that the virulence of the mutant was attenuated relative to that of the wild-type organism. These results suggest that dentilisin activity plays a major role in the structural organization of the outer sheath of T. denticola. The loss of dentilsin activity and the structural change in the outer sheath affect the pathogenicity of T. denticola.

REGISTRY NUMBERS: 37259-58-8D: SERINE PROTEASES
DESCRIPTORS:
MAJOR CONCEPTS: Enzymology (Biochemistry and Molecular Biophysics); Infection; Morphology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Spirochaetaceae--Spirochaetales, Spirochetes, Eubacteria, Bacteria, Microorganisms
ORGANISMS: *Fusobacterium*-nucleatum (Bacteroidaceae)--pathogen; Treponema-denticola (Spirochaetaceae)--pathogen
ORGANISMS: PARTS ETC: outer sheath--organization
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Microorganisms
CHEMICALS & BIOCHEMICALS: dentilisin--activity; serine proteases; DNA fragments
MISCELLANEOUS TERMS: bacterial ultrastructure; enzyme-deficient mutants ; pathogenicity; physiology
CONCEPT CODES:
36002 Medical and Clinical Microbiology-Bacteriology
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10804 Enzymes-Methods
12502 Pathology, General and Miscellaneous-General
19001 Dental and Oral Biology-General; Methods
30500 Morphology and Cytology of Bacteria
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
32000 Microbiological Apparatus, Methods and Media
32300 Microbiological Ultrastructure (1972-)
BIOSYSTEMATIC CODES:
06112 Spirochaetaceae (1992-)
06901 Bacteroidaceae (1992-)

9/9/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06944118 BIOSIS NO.: 000089066120
PROPOSAL OF THREE SUBSPECIES OF *FUSOBACTERIUM*-NUCLEATUM KNORR 1922 *FUSOBACTERIUM*-NUCLEATUM-SSP-NUCLEATUM NEW-SUBSPECIES NEW-COMBINATION *FUSOBACTERIUM*-NUCLEATUM-SSP-POLYMORPHUM NEW-SUBSPECIES NEW-COMBINATION REVIVED NAME AND *FUSOBACTERIUM*-NUCLEATUM-SSP-VINCENTII NEW-SUBSPECIES NEW-COMBINATION REVIVED NAME
AUTHOR: DZINK J L; SHEENAN M T; SOCRANSKY S S
AUTHOR ADDRESS: FORSYTH DENT. CENT., BOSTON, MASS. 02115.
JOURNAL: INT J SYST BACTERIOL 40 (1). 1990. 74-78. 1990
FULL JOURNAL NAME: International Journal of Systematic Bacteriology
CODEN: IJSBA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Heterogeneity among isolates of *Fusobacterium* nucleatum has been recognized for many years. The phenotypic properties of 340 strains considered to be F. nucleatum were examined. While these strains were phenotypically similar and fit the description of F. nucleatum, they could be differentiated into three groups on the basis of *electroporetic* patterns of whole-cell proteins and DNA homology. Strains in groups I and II showed > 80% DNA homology within groups and < 75% similarity between groups. Strains of group III demonstrated > 85% DNA homology to each other and < 65% similarity to strains in groups I and II. We propose that *Fusobacterium* nucleatum be divided into the following three subspecies: *Fusobacterium* nucleatum subsp. nucleatum, with type strain ATCC 25586; *Fusobacterium* nucleatum subsp. polymorphum, with type strain ATCC 10953; and *Fusobacterium* nucleatum subsp. vincentii, with type strain ATCC 49256.

DESCRIPTORS: *FUSOBACTERIUM*-POLYMORPHUM WHOLE CELL PROTEIN PATTERN DNA HOMOLOGY
CONCEPT CODES:
00504 General Biology-Taxonomy, Nomenclature and Terminology
30000 Bacteriology, General and Systematic
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
10010 Comparative Biochemistry, General
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
32000 Microbiological Apparatus, Methods and Media
BIOSYSTEMATIC CODES:
04910 Bacteroidaceae (1979-)
Microorganisms
Bacteria

9/9/4 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09822318 98348445 PMID: 9683480
Dentilisin activity affects the organization of the outer sheath of Treponema denticola.
Ishihara K; Kuramitsu HK; Miura T; Okuda K
Department of Microbiology, Oral Health Science Center, Tokyo Dental College, 1-2-2 Masago, Mihama-ku, Chiba 261-8502, Japan. ishihara@tdc.ac.jp
Journal of bacteriology (UNITED STATES) Aug 1998, 180 (15) p3837-44, ISSN 0021-9193 Journal Code: HH3
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
Prolyl-phenylalanine-specific serine protease (dentilisin) is a major extracellular protease produced by Treponema denticola. The gene, prtP, coding for the protease was recently cloned and sequenced (K. Ishihara, T. Miura, H. K. Kuramitsu, and K. Okuda, Infect. Immun. 64:5178-5186, 1996). In order to determine the role of this protease in the physiology and virulence of T. denticola, a dentilisin-deficient mutant, K1, was constructed following *electroporation* with a prtP-inactivated DNA fragment. No chymotrypsin-like protease activity was detected in the dentilisin-deficient mutant. In addition, the high-molecular-mass oligomeric protein characteristic of the outer sheath of the organism decreased in the mutant. Furthermore, the hydrophobicity of the mutant was decreased, and coaggregation of the mutant with *Fusobacterium* nucleatum was enhanced compared to that of the wild-type organism. The results obtained with a mouse abscess model system indicated that the virulence of the mutant was attenuated relative to that of the wild-type organism. These results suggest that dentilisin activity plays a major role in the structural organization of the outer sheath of T. denticola. The loss of dentilsin activity and the structural change in the outer sheath affect the pathogenicity of T. denticola.
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: *Cell Membrane--ultrastructure--UL; *Chymotrypsin --metabolism--ME; *Treponema--physiology--PH; Cell Membrane--physiology--PH

; Chymotrypsin--genetics--GE; Chymotrypsin--isolation and purification--IP
; Cloning, Molecular; Electrophoresis, Polyacrylamide Gel; Escherichia coli
--genetics--GE; *Fusobacterium*--genetics--GE; Immunoblotting; Mice;
Periodontal Abscess--microbiology--MI; Periodontal Abscess--physiopatholog
y--PP; Plasmids; Polymerase Chain Reaction; Porphyromonas gingivalis
--genetics--GE; Recombinant Proteins--biosynthesis--BI; Recombinant
Proteins--isolation and purification--IP; Recombinant Proteins--metabolism
--ME; Treponema--enzymology--EN; Treponema--genetics--GE; Treponema
--pathogenicity--PY; Treponemal Infections--physiopathology--PP; Virulence
CAS Registry No.: 0 (Plasmids); 0 (Recombinant Proteins)
Enzyme No.: EC 3.4.21.- (dentilisin); EC 3.4.21.1 (Chymotrypsin)
Record Date Created: 19980820
?s fusobacterium and plasmid?
6050 FUSOBACTERIUM
174177 PLASMID?
S10 40 FUSOBACTERIUM AND PLASMID?
?rd
...completed examining records
S11 28 RD (unique items)
?t/9/all

11/9/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12360222 BIOSIS NO.: 200000113724
Native *plasmids* of *Fusobacterium* nucleatum: Characterization and use in development of genetic systems.
AUTHOR: Kinder Haake Susan(a); Yoder Sean C; Attarian Gwynne; Podkaminer Kara
AUTHOR ADDRESS: (a)Section of Periodontics, UCLA School of Dentistry, 10833 Le Conte Ave., Los Angeles, CA, 90095-1668**USA
JOURNAL: Journal of Bacteriology 182 (4):p1176-1180 Feb., 2000
ISSN: 0021-9193
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

post filing date

ABSTRACT: Three native *plasmids* of *Fusobacterium* nucleatum were characterized, including DNA sequence analysis of one *plasmid*, pFN1. A shuttle *plasmid*, pHS17, capable of transforming Escherichia coli and F. nucleatum ATCC 10953 was constructed with pFN1. pHS17 was stably maintained in the F. nucleatum transformants, and differences in the transformation efficiencies suggested the presence of a restriction-modification system in F. nucleatum.

DESCRIPTORS:
MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Bacteroidaceae--Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Enterobacteriaceae--Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms
ORGANISMS: Escherichia coli (Enterobacteriaceae); *Fusobacterium* nucleatum (Bacteroidaceae)--strain-ATCC 10953
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Microorganisms
CHEMICALS & BIOCHEMICALS: pFN1--*Fusobacterium* nucleatum native *plasmid*, characterization, shuttle *plasmid*; pFN1. pHS17
METHODS & EQUIPMENT: DNA sequence analysis--analytical method, molecular genetic method
MISCELLANEOUS TERMS: restriction-modification system
CONCEPT CODES:
31500 Genetics of Bacteria and Viruses
10052 Biochemical Methods-Nucleic Acids, Purines and Pyrimidines
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
32000 Microbiological Apparatus, Methods and Media
10506 Biophysics-Molecular Properties and Macromolecules
31000 Physiology and Biochemistry of Bacteria
BIOSYSTEMATIC CODES:
06702 Enterobacteriaceae (1992-)

06901 Bacteroidaceae (1992-)

11/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12030651 BIOSIS NO.: 199900311170
Transformation of *Fusobacterium* nucleatum by electroporation.
AUTHOR: Haake S Kinder(a); Yoder S C(a)
AUTHOR ADDRESS: (a)School of Dentistry, UCLA, Los Angeles, CA**USA
JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 99p331 1999
CONFERENCE/MEETING: 99th General Meeting of the American Society for Microbiology Chicago, Illinois, USA May 30-June 3, 1999
SPONSOR: American Society for Microbiology
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
DESCRIPTORS:
MAJOR CONCEPTS: Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Bacteroidaceae--Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Enterobacteriaceae--Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms
ORGANISMS: E. coli {Escherichia coli} (Enterobacteriaceae); *Fusobacterium* nucleatum (Bacteroidaceae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Microorganisms
CHEMICALS & BIOCHEMICALS: pHS17--shuttle *plasmid*; DNA--transfer
METHODS & EQUIPMENT: electroporation--DNA transfer method
MISCELLANEOUS TERMS: Meeting Abstract; Meeting Poster
CONCEPT CODES:
31500 Genetics of Bacteria and Viruses
10050 Biochemical Methods-General
10060 Biochemical Studies-General
32000 Microbiological Apparatus, Methods and Media
31000 Physiology and Biochemistry of Bacteria
00520 General Biology-Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals
BIOSYSTEMATIC CODES:
06702 Enterobacteriaceae (1992-)
06901 Bacteroidaceae (1992-)

11/9/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11965428 BIOSIS NO.: 199900218741
Characterisation of a 5.5-kb cryptic *plasmid* present in different isolates of Bacteroides spp. originating from Hungary.
AUTHOR: Soki J; Szoke I; Nagy Elisabeth(a)
AUTHOR ADDRESS: (a)Department of Clinical Microbiology, Albert Szent-Gyorgyi Medical University, Szeged**Hungary
JOURNAL: Journal of Medical Microbiology 48 (1):p25-31 Jan., 1999
ISSN: 0022-2615
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: The *plasmid* profiles of 97 Bacteroides isolates collected during screening for different pathogenic markers of this genus were investigated. In all, 48% of 69 isolates from infections that belonged to six species harboured low mol. wt *plasmids* (2.8-11.0 kb). Similar *plasmids* were also found in 39% of 28 isolates, belonging to eight species, from faeces of healthy persons. The two most frequently obtained types were the 5.5- and the 4.2-kb *plasmids*, which were present in 70% and 52% of all *plasmid*-bearing isolates, respectively. Restriction endonuclease analysis revealed that the 5.5-kb *plasmids* found in the

different Bacteroides spp. exhibited the same restriction map, with the exception that pBVP61 lacked the PstI recognition site. The two *plasmid* types (4.2 and 5.5 kb) seem to be most widely distributed among Bacteroides isolates independent of the site of isolation and with some differences depending on geographic regions.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Infection
BIOSYSTEMATIC NAMES: Bacteroidaceae--Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Gram-Negative Aerobic Rods and Cocci--Eubacteria, Bacteria, Microorganisms; Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: human (Hominidae)--patient; Bacteroides spp. (Bacteroidaceae) --pathogen; Flavobacterium sp. (Gram-Negative Aerobic Rods and Cocci) --pathogen; *Fusobacterium* sp. (Bacteroidaceae)--pathogen; Porphyromonas sp. (Bacteroidaceae)--pathogen
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Animals; Bacteria; Chordates; Eubacteria; Humans; Mammals; Microorganisms; Primates; Vertebrates
CHEMICALS & BIOCHEMICALS: 5.5 kb cryptic *plasmid*
GEOGRAPHICAL NAME: Hungary (Europe, Palearctic region)
CONCEPT CODES:
36001 Medical and Clinical Microbiology-General; Methods and Techniques
10060 Biochemical Studies-General
30000 Bacteriology, General and Systematic
BIOSYSTEMATIC CODES:
06500 Gram-Negative Aerobic Rods and Cocci (1992-)
06901 Bacteroidaceae (1992-)
86215 Hominidae

11/9/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10927251 BIOSIS NO.: 199799548396
Cloning and expression of FomA, the major outer-membrane protein gene from *Fusobacterium* nucleatum T18.
AUTHOR: Haake Susan Kinder(a); Wang Xiurong
AUTHOR ADDRESS: (a)Section Periodontics, UCLA Sch. Dentistry, 10833 Le Conte Ave., Los Angeles, CA 90095-1668**USA
JOURNAL: Archives of Oral Biology 42 (1):p19-24 1997
ISSN: 0003-9969
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The major outer-membrane protein, FomA, of *Fusobacterium* nucleatum has been associated with porin activity, interbacterial adherence and stimulation of host immune cells. Until now, molecular analysis of FomA has not been possible because previous attempts to clone the fomA gene were not successful. The inability to clone F. nucleatum genes led to speculation that Escherichia coli may not be a suitable host. This report concerns the amplification of the fomA gene of F. nucleatum T18 using oligonucleotide primers containing restriction endonuclease sites that allow cloning of fomA into the E. coli expression vector pMMB67. The resultant *plasmid*, pXW1, was transformed into E. coli DH5-alpha, providing high-level expression of recombinant FomA (rFomA). Amino acid sequencing of rFomA demonstrated that the FomA signal peptide was correctly processed by E. coli signal peptidase I. rFomA was correctly localized to the outer membrane by the E. coli export pathway. The rFomA protein also displayed the heat-modifiable oligomeric and conformational properties of native FomA (nFomA). This demonstration of rFomA expression, processing, export, and secondary and tertiary structure in E. coli provides support for the feasibility of molecular analysis of the structure and function of FomA and other F. nucleatum proteins using recombinant techniques.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Membranes (Cell Biology); Methods and Techniques; Physiology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria; Enterobacteriaceae--Eubacteria, Bacteria

ORGANISMS: Escherichia coli (Enterobacteriaceae); *Fusobacterium* nucleatum (Bacteroidaceae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms
MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence
MISCELLANEOUS TERMS: Research Article; CLONING; EXPRESSION; EXPRESSION VECTOR; FOMA; GENE EXPRESSION; MOLECULAR GENETICS; OUTER MEMBRANE PROTEIN; OUTER-MEMBRANE PROTEIN GENE; PORIN; STRAIN-T18
CONCEPT CODES:
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10504 Biophysics-General Biophysical Techniques
10506 Biophysics-Molecular Properties and Macromolecules
10508 Biophysics-Membrane Phenomena
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
BIOSYSTEMATIC CODES:
06702 Enterobacteriaceae (1992-)
06901 Bacteroidaceae (1992-)

11/9/5 (Item 5 from file: 5)

10696762 BIOSIS NO.: 199799317907
Cloning of the fomA gene, encoding the major outer membrane porin of *Fusobacterium* nucleatum ATCC10953.
AUTHOR: Jensen H B; Skeidsvoll J; Fjellbirkeland A; Hogh B; Puntervoll P; Kleivdal H; Tommassen J(a)
AUTHOR ADDRESS: (a)Dep. Biochem. Mol. Biol., Univ. Bergen, Aarstadveien 19, N-5009 Bergen**Norway
JOURNAL: Microbial Pathogenesis 21 (5):p331-342 1996
ISSN: 0882-4010
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The major outer membrane protein, FomA, of the Gram-negative human oral pathogen *Fusobacterium* nucleatum functions as a porin and is assumed to act as a receptor protein in coaggregation with other oral pathogenic bacteria such as Streptococcus sanguis and Porphyromonas gingivalis. We describe here the cloning of fomA from F. nucleatum in E. coli. Using pGEM3Zf(+), three recombinant *plasmids* were carrying parts of the fomA gene, but none of these contained regions upstream of the coding sequence. From these *plasmids* a clone was constructed which contained the whole fomA gene. The ATCC 10953 fomA gene was cloned under the phosphate limitation-inducible phoE promoter, using a vector derived from pACYC184. The protein was found to be incorporated into the outer membrane of the host in an apparently normal manner, as judged by heat-modifiability, trypsin-accessibility, and accessibility to antibodies to the protein in a whole cell enzyme-linked immunosorbent assay. The cloned FomA was found to exhibit pore-forming activity.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Cell Biology; Dental and Oral System (Ingestion and Assimilation); Genetics; Infection; Membranes (Cell Biology); Metabolism; Methods and Techniques ; Molecular Genetics (Biochemistry and Molecular Biophysics); Pathology ; Physiology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria
ORGANISMS: *Fusobacterium* nucleatum (Bacteroidaceae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms
MISCELLANEOUS TERMS: Research Article; CELL BIOLOGY; CLONING; ENCODES MAJOR OUTER MEMBRANE PORIN; FOMA GENE; INFECTION; MOLECULAR GENETICS; ORAL PATHOGENS; OUTER MEMBRANE PROTEINS; PORE-FORMING ACTIVITY; PORINS; RECOMBINANT *PLASMIDS*; STRAIN-ATCC10953
CONCEPT CODES:
10052 Biochemical Methods-Nucleic Acids, Purines and Pyrimidines
10054 Biochemical Methods-Proteins, Peptides and Amino Acids
10300 Replication, Transcription, Translation
10506 Biophysics-Molecular Properties and Macromolecules

10508 Biophysics-Membrane Phenomena
12502 Pathology, General and Miscellaneous-General
13012 Metabolism-Proteins, Peptides and Amino Acids
19006 Dental and Oral Biology-Pathology
30500 Morphology and Cytology of Bacteria
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
36002 Medical and Clinical Microbiology-Bacteriology
BIOSYSTEMATIC CODES:
06901 Bacteroidaceae (1992-)

11/9/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10368495 BIOSIS NO.: 199698823413
Structural organization of pRAM4, a cryptic *plasmid* from Prevotella ruminicola.
AUTHOR: Ogata Koretsugu; Aminov Rustem I(a); Nagamine Takafumi; Benno Yoshimi; Sezaki Tsutomu; Mitsumori Makoto; Minato Hajime; Itabashi Hisao
AUTHOR ADDRESS: (a)STAFF-Inst., Tsukuba 305**Japan
JOURNAL: Plasmid 35 (2):p91-97 1996
ISSN: 0147-619X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A total of 530 strains of rumen bacteria were screened for the presence of *plasmid* DNA. The percentage of *plasmid*-bearing strains was found to be the highest among the Bacteroides/Prevotella group (9.9%), while it was less than 1% in the Butyrivibrio (0.2%) and Clostridium (0.6%) genera. A small cryptic *plasmid* pRAM4 from Prevotella ruminicola T31 was subcloned in Escherichia coli and completely sequenced. Two open reading frames, encoding potential polypeptides of M-r 32,322 (ORF1) and 32,122 (ORF2) with limited sequence similarity to replication initiation and mobilization proteins, respectively, could be identified within the sequence. The region upstream from ORF1 had an AT-rich (75%) region followed by four 22-bp direct repeats, a structure characteristic of replication origins. The *plasmid* hybridized at high stringency with *plasmids* from Bacteroides/Prevotella and Butyrivibrio, and with pBR322 suggesting that at least regions of the *plasmid* are widespread.

REGISTRY NUMBERS: 167207-41-2: GENBANK-U30294
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Physiology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria; Endospore-forming Gram-Positives--Eubacteria, Bacteria; Gram-Positive Cocci--Eubacteria, Bacteria; Irregular Nonsporing Gram-Positive Rods--Eubacteria, Bacteria; Regular Nonsporing Gram-Positive Rods--Eubacteria , Bacteria; Veillonellaceae--Eubacteria, Bacteria
ORGANISMS: endospore-forming gram-positive rods and cocci (Endospore-forming Gram-Positives); gram-positive cocci (Gram-Positive Cocci); irregular nonsporing gram-positive rods (Irregular Nonsporing Gram-Positive Rods); regular nonsporing gram-positive rods (Regular Nonsporing Gram-Positive Rods); Bacteroides (Bacteroidaceae); Bifidobacterium (Irregular Nonsporing Gram-Positive Rods); Butyrivibrio (Irregular Nonsporing Gram-Positive Rods); Clostridium (Endospore-forming Gram-Positives); Eubacterium (Irregular Nonsporing Gram-Positive Rods); Fibrobacter succinogenes (Bacteroidaceae); *Fusobacterium* (Bacteroidaceae); Lactobacillus (Regular Nonsporing Gram-Positive Rods); Megasphaera (Veillonellaceae); Peptostreptococcus (Gram-Positive Cocci); Prevotella ruminicola (Bacteroidaceae); Propionibacterium (Irregular Nonsporing Gram-Positive Rods); Ruminobacter amylophilus (Bacteroidaceae); Ruminococcus albus (Gram-Positive Cocci
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms
CHEMICALS & BIOCHEMICALS: GENBANK-U30294

MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; molecular sequence data; nucleotide sequence; GENBANK-U30294
MISCELLANEOUS TERMS: DNA COMPARISON; MOBILIZATION PROTEIN; PBR322; REPLICATION INITIATION PROTEIN; REPLICATION ORIGIN
CONCEPT CODES:
03502 Genetics and Cytogenetics-General
10010 Comparative Biochemistry, General
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
BIOSYSTEMATIC CODES:
06901 Bacteroidaceae (1992-)
07001 Veillonellaceae (1992-)
07700 Gram-Positive Cocci (1992-)
07810 Endospore-forming Gram-Positives (1992-)
07830 Regular Nonsporing Gram-Positive Rods (1992-)
08890 Irregular Nonsporing Gram-Positive Rods (1992-)

11/9/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09974676 BIOSIS NO.: 199598429594
Insertional inactivation of binding determinants of Streptococcus crista CC5A using Tn916.
AUTHOR: Correia F F; Dirienzo J M; Lamont R J; Anderman C; McKay T L; Rosan Burton(a)
AUTHOR ADDRESS: (a)Dep. Microbiol., Sch. Dent. Med., Univ. Pa., 4001 Spruce St., Philadelphia, PA 19104-6002**USA
JOURNAL: Oral Microbiology and Immunology 10 (4):p220-226 1995
ISSN: 0902-0055
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Intermicrobial binding plays an important role in the ecology of the oral cavity because it represents one mechanism by which specific bacteria colonize dental plaque. The formation of "corncobs", a morphologically distinct microbial unit composed of Streptococcus crista and *Fusobacterium* nucleatum, is a highly specific binding interaction that depends on the presence of polar tufts of fimbriae on the streptococci. We have used a genetic approach to examine the role of streptococcal cell surface components involved in the binding of S. crista to F. nucleatum. Such binding may be an important component of corncob formation. A method for the genetic transformation of S. crista was used to transfer the broad host range transposon, Tn916, into the bacteria. Cells were grown to early log phase in brain heart infusion broth containing 10% fetal calf serum. The competent cells were mixed with purified DNA from pDL916, a *plasmid* construct consisting of Tn916 and the streptococcal/Escherichia coli shuttle vector pDL278. Over 300 transformants were screened for a reduction in binding to F. nucleatum. Five of the transformants showed a change in binding ranging from 59% to 29% of the positive control values. Southern blots revealed that the binding-deficient transformants contained the Tn916 element integrated into one of 4 different sites in the chromosome. The transposon, integrated into 4 different sites, appeared to be stable in the absence of selective pressure. Based on these findings, it appears that some strains of S. crista are naturally competent and that insertional inactivation methods can be used to facilitate the study of binding receptors in this group of oral streptococci.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Membranes (Cell Biology); Physiology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria; Gram-Positive Cocci--Eubacteria, Bacteria
ORGANISMS: gram-positive cocci (Gram-Positive Cocci); *Fusobacterium* nucleatum (Bacteroidaceae); Streptococcus crista (Gram-Positive Cocci
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria;

microorganisms
MISCELLANEOUS TERMS: BINDING RECEPTOR; CELL SURFACE COMPONENT; DNA TRANSFER
CONCEPT CODES:
10506 Biophysics-Molecular Properties and Macromolecules
10508 Biophysics-Membrane Phenomena
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
BIOSYSTEMATIC CODES:
06901 Bacteroidaceae (1992-)
07700 Gram-Positive Cocci (1992-)

11/9/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09730705 BIOSIS NO.: 199598185623
Mobile genetic elements of *Fusobacterium* nucleatum.
AUTHOR: McKay Terry L; Ko Julie; Bilalis Yioryos; Dirienzo Joseph M(a)
AUTHOR ADDRESS: (a)Dep. Microbiol., Univ. Pa., Sch. Dent. Med., 4001 Spruce St., Philadelphia, PA 19104-6002**USA
JOURNAL: Plasmid 33 (1):p15-25 1995
ISSN: 0147-619X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The gram-negative anaerobic bacterium, *Fusobacterium* nucleatum, is a predominant member of the human oral flora. As a major component of subgingival plaque, this bacterium has a significant impact on the ecology of the oral cavity due to its ability to adhere to many different microbial species. The objective of this study was to identify and characterize *plasmids* and transposons that may have the potential to be developed into tools for cloning, genetic transformation, and mutagenesis of oral isolates of F. nucleatum. Analysis of a collection of laboratory strains resulted in the identification of a homologous family of small cryptic *plasmids*. *Plasmids* within this family ranged in size from 6.0 to 6.6 kb. Eighteen percent of all strains examined (n = 74) contained DNA sequences related to the *plasmids*. Homologous *plasmid* sequences were found in strains belonging to 2 of the 3 subspecies of the bacterium. The 2 smallest *plasmid* species were cloned in Escherichia coli to facilitate endonuclease restriction mapping. Among the strains examined for *plasmids*, 5 exhibited resistance to at least 10 mu-g/ml of tetracycline. These strains, all members of the subsp. polymorphum, contained a tetracycline resistance determinant (TetM) as part of a Tn916-like integrated transposon sequence. The Tn916-like element and 1 of the *plasmid* species co-resided in a single strain of the bacterium. Hybridization patterns of the Tn916-like sequences were identical in all 5 tetracycline-resistant strains. However, these strains appeared to be clonally distinct based on genomic fingerprinting.

REGISTRY NUMBERS: 60-54-8: TETRACYCLINE
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Pharmacology; Physiology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria; Hominidae--Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISMS: *Fusobacterium* nucleatum nucleatum (Bacteroidaceae); *Fusobacterium* nucleatum polymorphum (Bacteroidaceae); *Fusobacterium* nucleatum vincentii (Bacteroidaceae); Hominidae (Hominidae
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): animals; bacteria; chordates; eubacteria; humans; mammals; microorganisms; primates; vertebrates
CHEMICALS & BIOCHEMICALS: TETRACYCLINE
MISCELLANEOUS TERMS: HUMAN ORAL CAVITY; TETRACYCLINE RESISTANCE GENE; TN916-LIKE INTEGRATED TRANSPOSON SEQUENCE
CONCEPT CODES:
03502 Genetics and Cytogenetics-General
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
22002 Pharmacology-General

31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
19006 Dental and Oral Biology-Pathology
36002 Medical and Clinical Microbiology-Bacteriology
BIOSYSTEMATIC CODES:
06901 Bacteroidaceae (1992-)
86215 Hominidae

11/9/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09445759 BIOSIS NO.: 199497454129
Sequence variability of the 40-kDa outer membrane proteins of *Fusobacterium* nucleatum strains and a model for the topology of the proteins.
AUTHOR: Bolstad Anne Isine(a); Tommassen Jan; Jensen Harald B
AUTHOR ADDRESS: (a)Dep. Biochem. Mol. Biol., Lab. Oral Microbiol., Univ. Bergen, Arstadveien 19, 5009 Bergen**Norway
JOURNAL: Molecular & General Genetics 244 (1):p104-110 1994
ISSN: 0026-8925
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The complete nucleotide sequences of the fomA genes encoding the 40-kDa outer membrane proteins (OMPs) of strains ATCC 10953 and ATCC 25586 of *Fusobacterium* nucleatum were determined using the genomic DNA, or DNA fragments ligated into a vector *plasmid*, as template in a polymerase chain reaction. The deduced amino acid sequences of these two proteins were aligned with the amino acid sequence of the corresponding protein of F. nucleatum strain Fev1 and examined for conserved/variable polypeptide segments. A model for the topology of the 40-kDa OMPs is proposed on the basis of this alignment and application of the structural principles derived for OMPs of Escherichia coli. According to this model, sixteen polypeptide segments, which are highly conserved, traverse the outer membrane, thereby creating eight external loops, most of which are highly variable.

REGISTRY NUMBERS: 8027-51-8: AMINO CID
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Membranes (Cell Biology); Physiology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria
ORGANISMS: *Fusobacterium* nucleatum (Bacteroidaceae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms
CHEMICALS & BIOCHEMICALS: AMINO CID
MOLECULAR SEQUENCE DATABANK NUMBER: amino acid sequence; molecular sequence data; nucleotide sequence; EMBL-X72582; EMBL-X72583
MISCELLANEOUS TERMS: DNA; FOMA GENE
CONCEPT CODES:
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10508 Biophysics-Membrane Phenomena
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
BIOSYSTEMATIC CODES:
06901 Bacteroidaceae (1992-)

11/9/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09257787 BIOSIS NO.: 199497266157
Comparative antibacterial spectrum of trimethoprim and brodimoprim.
AUTHOR: Amyes S G B
AUTHOR ADDRESS: Scottish Antibiotic Reference Lab., Dep. Med. Microbiol., Med. Sch., Univ. Edinburgh, Teviot Place, **UK

JOURNAL: Journal of Chemotherapy 5 (6):p417-421 1993
ISSN: 1120-009X
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Brodimoprim is a new 2,4-diaminobenzylpyrimidine that selectively inhibits bacterial and resistance *plasmid* dihydrofolate reductases to a similar or greater extent than trimethoprim. Brodimoprim reaches equivalent levels in the serum as trimethoprim for the same dosage regimens but, unlike trimethoprim, brodimoprim has a long half-life. Brodimoprim has a similar antibacterial spectrum to trimethoprim against bacterial species normally sensitive to this class of drugs although it is not active against aerobic bacteria that are normally inherently trimethoprim-resistant, such as Pseudomonas spp. Against a range of strains of the Enterobacteriaceae trimethoprim was slightly more active, although in an in vivo murine model brodimoprim had a significantly better cure rate. Brodimoprim was 2 - 4-fold more active against several strains of Neisseria, Nocardia, Vibrio cholerae, Bacteroides and other anaerobes. In particular the MIC-90 values of brodimoprim for Clostridium and *Fusobacterium* spp were lower than those of trimethoprim.

REGISTRY NUMBERS: 738-70-5: TRIMETHOPRIM; 56518-41-3: BRODIMOPRIM;
9002-03-3: DIHYDROFOLATE REDUCTASE
DESCRIPTORS:
MAJOR CONCEPTS: Enzymology (Biochemistry and Molecular Biophysics); Pharmacology; Physiology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria; Endospore-forming Gram-Positives--Eubacteria, Bacteria; Enterobacteriaceae--Eubacteria, Bacteria; Neisseriaceae--Eubacteria, Bacteria; Nocardioform Actinomycetes--Eubacteria, Bacteria; Vibrionaceae--Eubacteria, Bacteria
ORGANISMS: endospore-forming gram-positive rods and cocci (Endospore-forming Gram-Positives); Bacteroides (Bacteroidaceae); Clostridium (Endospore-forming Gram-Positives); Enterobacteriaceae (Enterobacteriaceae); *Fusobacterium* (Bacteroidaceae); Neisseria (Neisseriaceae); Nocardia (Nocardioform Actinomycetes); Nocardioform actinomycetes (Nocardioform Actinomycetes); Vibrio cholerae (Vibrionaceae
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms
CHEMICALS & BIOCHEMICALS: TRIMETHOPRIM; BRODIMOPRIM; DIHYDROFOLATE REDUCTASE
MISCELLANEOUS TERMS: ANTIBACTERIAL-DRUG; BRODIMOPRIM; DIHYDROFOLATE REDUCTASE; ENZYME INHIBITOR-DRUG; MINIMUM INHIBITORY CONCENTRATION; TRIMETHOPRIM
CONCEPT CODES:
10808 Enzymes-Physiological Studies
22002 Pharmacology-General
31000 Physiology and Biochemistry of Bacteria
38504 Chemotherapy-Antibacterial Agents
10060 Biochemical Studies-General
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
BIOSYSTEMATIC CODES:
06507 Neisseriaceae (1992-)
06702 Enterobacteriaceae (1992-)
06704 Vibrionaceae (1992-)
06901 Bacteroidaceae (1992-)
07810 Endospore-forming Gram-Positives (1992-)
08810 Nocardioform Actinomycetes (1992-)

11/9/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08937255 BIOSIS NO.: 199396088756
OXA-11, an extended-spectrum variant of OXA-10 (PSE-2) beta-lactamase from Pseudomonas aeruginosa.
AUTHOR: Hall L M C(a); Livermore D M; Gur D; Akova M; Akalin H E

AUTHOR ADDRESS: (a)Dep. Med. Microbiology, London Hosp. Med. Coll., Turner Street, London E1 2AD**UK
JOURNAL: Antimicrobial Agents and Chemotherapy 37 (8):p1637-1644 1993
ISSN: 0066-4804
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Pseudomonas aeruginosa ABD, which was isolated in October 1991 from blood cultures of a burn patient in Turkey, was resistant to cephalosporins, particularly ceftazidime (MIC, 512 mu-g/ml), penicillins, aztreonam, and meropenem, but not to imipenem. Cephalosporin and penicillin resistance transferred to P. aeruginosa PU21 and was associated with a beta-lactamase with a pI of 6.4 encoded by a 100-MDa *plasmid* designated pMLH52. Like extended-spectrum TEM and SHV beta-lactamases, this enzyme hydrolyzed penicillins and newer cephalosporins but did not hydrolyze cefoxitin or carbapenems. However, it differed from TEM and SHV derivatives in being a potent oxacillinase, and its encoding gene did not hybridize with probes to TEM and SHV genes. To characterize the enzyme, libraries of total DNA were cloned into *plasmid* pUC19 and were transformed into Escherichia coli DH5-alpha. Recombinant *plasmids* that gave ceftazidime resistance all contained a 3.65-kb BamHl fragment. Deletions from this fragment allowed the beta-lactamase gene to be located on a 1.4-kb section of DNA, which contained an open reading frame of 798 bases. This encoded a protein that was deduced to differ from PSE-2 beta-lactamase only in having serine instead of asparagine at position 143 and aspartate instead of glycine at position 157. It is concluded that the resistance of isolate ABD depended on an extended-spectrum variant of the PSE-2 enzyme. The ability of this enzyme to cause ceftazidime resistance depended primarily on a low K-m for the compound; V-max remained low. It is proposed that PSE-2 should be transferred to the OXA group as OXA-10 and that the new enzyme be designated OXA-11.

REGISTRY NUMBERS: 72558-82-8: CEFTAZIDIME; 1406-05-9: PENICILLIN; 78110-38-0: AZTREONAM; 96036-03-2: MEROPENEM
DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Enzymology (Biochemistry and Molecular Biophysics); Genetics; Infection; Pharmacology
BIOSYSTEMATIC NAMES: Bacteria-General Unspecified--Eubacteria, Bacteria; Bacteroidaceae--Eubacteria, Bacteria; Endospore-forming Gram-Positives --Eubacteria, Bacteria; Gram-Positive Cocci--Eubacteria, Bacteria; Pseudomonadaceae--Eubacteria, Bacteria
ORGANISMS: Bacteroides fragilis (Bacteroidaceae); Clostridium (Endospore-forming Gram-Positives); *Fusobacterium* (Bacteroidaceae); Gram-negative bacteria (Bacteria - General Unspecified); Peptostreptococcus (Gram-Positive Cocci); Porphyromonas (Bacteroidaceae); Prevotella (Bacteroidaceae); Pseudomonadaceae (Pseudomonadaceae
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms
CHEMICALS & BIOCHEMICALS: CEFTAZIDIME; PENICILLIN; AZTREONAM; MEROPENEM
MISCELLANEOUS TERMS: ANTIBACTERIAL-DRUG; MINIMUM INHIBITORY CONCENTRATION
CONCEPT CODES:
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10806 Enzymes-Chemical and Physical
22002 Pharmacology-General
31500 Genetics of Bacteria and Viruses
36002 Medical and Clinical Microbiology-Bacteriology
38504 Chemotherapy-Antibacterial Agents
10060 Biochemical Studies-General
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10506 Biophysics-Molecular Properties and Macromolecules
BIOSYSTEMATIC CODES:
06508 Pseudomonadaceae (1992-)

08913392 BIOSIS NO.: 199396064893
Species-specific recombinant DNA probes for Mycoplasma meleagridis.
AUTHOR: Zhao Shaohua; Yamamoto Richard
AUTHOR ADDRESS: Dep. Epidemiol. and Preventive Med., Sch. Vet. Med., Univ. Calif., Davis, CA 95616**USA
JOURNAL: Veterinary Microbiology 35 (1-2):p179-185 1993
ISSN: 0378-1135
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Two recombinant DNA probes (pMM-2 and pMM-13) were isolated from a Mycoplasma meleagridis strain 17529 genomic library prepared in *plasmid* pUC8, and Escherichia coli strain JM83. In dot blot assays, 32P-labeled pMM-13 with a DNA insert of 3.5 kbp, hybridized with 18 isolates of M. meleagridis but not with 16 other known species of avian mycoplasmas. Except for weaker signals on hybridization with the M. meleagridis cultures, pMM-2 with an DNA insert of 0.85 kbp, showed a similar reaction pattern. The minimal concentration of M. meleagridis strain 17529 chromosomal DNA that pMM-13 and pMM-2 detected were 1 and 8 ng, respectively. Neither probe hybridized with chromosomal DNA of M. gallisepticum strain S6, M. synoviae strain WVU-1853, or M. iowae strain I-695 at concentration of 256 ng.

DESCRIPTORS:
MAJOR CONCEPTS: Genetics; Infection; Pathology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria; Micrococcaceae --Eubacteria, Bacteria; Mycoplasmataceae--Eubacteria, Bacteria
ORGANISMS: *Fusobacterium* necrophorum (Bacteroidaceae); Mycoplasmataceae (Mycoplasmataceae); Staphylococcus aureus (Micrococcaceae
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms
MISCELLANEOUS TERMS: BIOVAR A; BIOVAR B; FATALITY; INFECTIVITY ENHANCEMENT; LESION SEVERITY; LIVER LESIONS; MOUSE VIRULENCE; VETERINARY INFECTION
CONCEPT CODES:
12504 Pathology, General and Miscellaneous-Diagnostic
31500 Genetics of Bacteria and Viruses
36002 Medical and Clinical Microbiology-Bacteriology
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
BIOSYSTEMATIC CODES:
07512 Mycoplasmataceae (1992-)

11/9/13 (Item 13 from file: 5)

07057641 BIOSIS NO.: 000089127745
CHARACTERIZATION OF THE TET M DETERMINANTS IN UROGENITAL AND RESPIRATORY BACTERIA
AUTHOR: ROBERTS M C
AUTHOR ADDRESS: DEP. PATHOBIOL., SCH. PUBLIC HEALTH COMMUNITY MED., UNIV. WASHINGTON, SEATTLE, WASH. 98195.
JOURNAL: ANTIMICROB AGENTS CHEMOTHER 34 (3). 1990. 476-478. 1990
FULL JOURNAL NAME: Antimicrobial Agents and Chemotherapy
CODEN: AMACC
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Tetracycline-resistant *Fusobacterium* nucleatum, Haemophilus ducreyi, Mycoplasma hominis, Peptostreptococcus spp., Ureaplasma urealyticum, and Veillonella parvula had DNA sequences which showed homology throughout the length of the Tet M transposon, Tn916. In contrast, Gardnerella vaginilis, commensal Neisseria spp., and the 25.2-megadalton *plasmid* family lacked the complete transposon.

DESCRIPTORS: *FUSOBACTERIUM*-NUCLEATUM HAEMOPHILUS-DUCREYI MYCOPLASMA-HOMINIS PEPTOSTREPTOCOCCUS UREAPLASMA-UREALYTICUM

VEILLONELLA-PARVULA GARDNERELLA-VAGINALIS NEISSERIA TETRACYCLINE
ANTIBACTERIAL-DRUG TRANSPOSON
CONCEPT CODES:
  15506 Urinary System and External Secretions-Pathology
  16006 Respiratory System-Pathology
  31500 Genetics of Bacteria and Viruses
  36002 Medical and Clinical Microbiology-Bacteriology
  38504 Chemotherapy-Antibacterial Agents
  10060 Biochemical Studies-General
BIOSYSTEMATIC CODES:
  04814 Gram-negative Facultatively Anaerobic Rods-Uncertain Affiliation
         (1979-)
  04910 Bacteroidaceae (1979-)
  05110 Neisseriaceae (1979-)
  05210 Veillonellaceae (1979-)
  05512 Peptococcaceae (1979-)
  09112 Mycoplasmataceae (1979-)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA):
  Microorganisms
  Bacteria

11/9/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06094083 BIOSIS NO.: 000085057232
DETECTION OF *PLASMID* DNA IN PERIODONTOPATHIC BACTERIA
AUTHOR: SAKO K; KATO T; ONO M; ISHIHARA K; OHTA K; TAKAZOE I; OKUDA K
AUTHOR ADDRESS: DEP. MICROBIOL., TOKYO DENTAL COLL., 1-2-2 MASAGO, CHIBA,
  260 JPN.
JOURNAL: BULL TOKYO DENT COLL 28 (3). 1987. 129-136. 1987
FULL JOURNAL NAME: Bulletin of Tokyo Dental College
CODEN: BTDCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A total of 217 gram-negative bacteria, including black and
  non-pigmented Bacteroides, *Fusobacterium* nucleatum, Capnocytophaga
  species and Haemophilus actinomycetemcomitans, mainly isolated from human
  oral cavities, were examined for their *plasmid* DNA content. *Plasmid*
  DNA was detected in 7 strains of 134 Bacteroides, 15 strains of 33 R.
  nucleatum, 7 strains of 14 Capnocytophaga species and 4 strains of 36 H.
  actinomycetemcomitans. No positive correlation was found bewteen the
  plasmid DNA content and antibiotic resistance.

DESCRIPTORS: BACTEROIDES *FUSOBACTERIUM*-NUCLEATUM CAPNOCYTOPHAGA-SPP
HAEMOPHILUS-ACTINOMYCETEMCOMITANS ANTIBIOTIC RESISTANCE CODING
CONCEPT CODES:
  10300 Replication, Transcription, Translation
  19006 Dental and Oral Biology-Pathology
  22020 Pharmacology-Integumentary System, Dental and Oral Biology
  31000 Physiology and Biochemistry of Bacteria
  31500 Genetics of Bacteria and Viruses
  36002 Medical and Clinical Microbiology-Bacteriology
  38504 Chemotherapy-Antibacterial Agents
  10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
BIOSYSTEMATIC CODES:
  04814 Gram-negative Facultatively Anaerobic Rods-Uncertain Affiliation
         (1979-)
  04910 Bacteroidaceae (1979-)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA):
  Microorganisms
  Bacteria

11/9/15 (Item 15 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05664173 BIOSIS NO.: 000084012578

IN-VITRO ACTIVITY AND BETA LACTAMASE STABILITY OF A NEW PENEM CGP-31608
AUTHOR: NEU H C; CHIN N-X; NEU N M
AUTHOR ADDRESS: DEP. MED., COLL. PHYSICIANS SURG., COLUMBIA UNIV., NEW YORK, N.Y. 10032.
JOURNAL: ANTIMICROB AGENTS CHEMOTHER 31 (4). 1987. 558-569. 1987
FULL JOURNAL NAME: Antimicrobial Agents and Chemotherapy
CODEN: AMACC
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The in vitro activity of CGP 31608, a new penem, against aerobic and anaerobic organisms was evaluated and compared with those of other beta-lactams. CGP 31608 inhibited Escherichia coli, Klebsiella pneumoniae, K. oxytoca, Proteus mirabilis, Citrobacter diversus, and Salmonella, Shigella, Aeromonas, and Yersinia spp. with MICs for 50% of the strains (MIC50S) of 2 to 4 .mu.g/ml and MIC90S of 4 .mu.g/ml, compared with cefotaxime, ceftazidime, aztreonam, and imipenem MICs of < 0.25 .mu.g/ml. MIC90S were 8 .mu.g/ml for Enterobacter species and C. freudii, for which other agents had MICs of 32 .mu.g/ml, except imipenem, which had equal activity. The MIC90 for Proteus vulgaris, Morganella morganii, Providencia stuartii, and Providencia rettgeri was 8 .mu.g/ml, compared with <2 .mu.g/ml shown by the other agents. Acinetobacter species resistant to other agents except imipenem were inhibited by 4 .mu.g/ml, as were Pseudomonas aeruginosa, including piperacillin-, ceftazidime-, and gentamicin-resistant isolates. The MIC for P. cepacia, P. fluorescens, and P. acidovorans was .ltoreq. 8 .mu.g/ml, but that for P. maltophilia was .gtoreq. 128 .mu.g/ml. Hemolytic streptococci A, B, C, G, and F were inhibited by < 1 .mu.g/ml, but the MIC for Streptococcus faecalis was .gtoreq. 32 .mu.g/ml. MICs for Staphylococcus aureus methicillin-susceptible and -resistant strains were .ltoreq. 1 .mu.g/ml, as were those for methicillin-susceptible and -resistant S. epidermidis. Bacteroides fragilis and Clostridium species and *Fusobacterium* spp. were inhibited by .ltoreq. 4 .mu.g/ml. CGP 31608 was not hydrolyzed by *plasmid* beta-lactamases TEM-1, TEM-2, SHV-1, PSE-1, OXA-2, PSE-4, or by S. aureus. Chromosomal beta-lactamases of type Ia in Enterobacter cloacae P99 and Morganella morganii, Ic in P. vulgaris, K-1 in K. oxytoca, and Id in P. aeruginosa also did not hydrolyze CGP 31608. It inhibited TEM-1, but the 50% inhibitory concentration was 14.2 .mu.g/ml compared with 0.15 .mu.g/ml for the P99 enzyme. CGP 31608 induced beta-lactamases in P. aeruginosa, E. cloacae, C. freudii and Providencia rettgeri, but there was no increase in MICs for the isolates and it did not select strains derepressed for beta-lactamase production. Synergy of CGP 31608 and gentamicin was found against 90% P. aeruginosa, 60% Enterobacter cloacae, and 50% Serratia marcescens strains. No synergy was found with rifamipin. A postantibiotic effect was found against E. coli.

DESCRIPTORS: CEFOTAXIME CEFTAZIDIME AZTREONAM IMIPENEM METHICILLIN GENTAMICIN RIFAMPIN ANTIBACTERIAL-DRUG ANTIBIOTICS
CONCEPT CODES:
36002 Medical and Clinical Microbiology-Bacteriology
38504 Chemotherapy-Antibacterial Agents
10060 Biochemical Studies-General
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10068 Biochemical Studies-Carbohydrates
10808 Enzymes-Physiological Studies
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
32600 In Vitro Studies, Cellular and Subcellular

05558305 BIOSIS NO.: 000083031445
IN-VITRO ACTIVITY AND BETA LACTAMASE STABILITY OF A NEW DIFLUORO OXACEPHEM 6315-S
AUTHOR: NEU H C; CHIN N-X
AUTHOR ADDRESS: DEP. OF MED., COLL. OF PHYSICIANS AND SURGEONS, COLUMBIA UNIV., NEW YORK, NY 10032.
JOURNAL: ANTIMICROB AGENTS CHEMOTHER 30 (5). 1986. 638-644. 1986

FULL JOURNAL NAME: Antimicrobial Agents and Chemotherapy
CODEN: AMACC
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: 6315-S, a novel difluoromethyl thioacetamido oxacephem, had in vitro activity comparable to that of cefotaxime and moxalactam against Escherichia coli Klebsiella pneumoniae, Proteus mirabilis, Klebsiella oxytoca, Citrobacter diversus, Salmonella spp., and Shigella spp., inhibiting 90% at .ltoreq. 0.25 .mu.g/ml. It inhibited piperacillin- and cefoperazone-resistant isolates in these species. 6315-S did not inhibit cefotaxime- or moxalactam-resistant Citrobacter freundii, Enterobacter aerogenes, or Enterobacter cloacae (MICs for 90% of the strains tested were .gtoreq. 16 .mu.g/ml). Proteus vulgaris resistant to cefotaxime was inhibited. Pseudomonas species and Acinetobacter species were resistant (MICs > 64 .mu.g/ml) MICs for 90% of the Staphylococcus aureus and S. epidermidis isolates were 4 .mu.g/ml. 6315-S was highly active against anaerobic species of Clostridium, *Fusobacterium*, Bacteroides, and peptostreptococci and was superior to other agents against these organisms. 6315-s was not hydrolyzed by the major *plasmid* and chromosomal beta-lactamases, but it induced chromosomal beta-lactamases in Enterobacter cloacae and Pseudomonas aeruginosa.

DESCRIPTORS: 7-BETA
DIFLUOROMETHYLTHIOACETAMIDO-7-ALPHA-METHOXY-3-1-HYDROETHYL-1H-TETRAZOL-5-YL
THIOMETHYL-1-OXA-3-CEPHEM-4-CARBOXYLIC ACID ANTIBACTERIAL-DRUG ANTIBIOTICS
CONCEPT CODES:
  22002 Pharmacology-General
  36002 Medical and Clinical Microbiology-Bacteriology
  38504 Chemotherapy-Antibacterial Agents
  10060 Biochemical Studies-General
  10064 Biochemical Studies-Proteins, Peptides and Amino Acids
  10808 Enzymes-Physiological Studies
  31000 Physiology and Biochemistry of Bacteria
  31500 Genetics of Bacteria and Viruses
  32600 In Vitro Studies, Cellular and Subcellular

11/9/17 (Item 17 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

04488838 BIOSIS NO.: 000029011875
PLASMID IN *FUSOBACTERIUM*-NECROPHORUM
AUTHOR: NAKAMURA K; HARASAWA R; SHINJO T
AUTHOR ADDRESS: DEP. VET. MICROBIOL., FAC. AGRIC., MIYAZAKI UNIV., 7710 KUMANO, MIYAZAKI 889-21, JPN.
JOURNAL: JPN J VET SCI 47 (2). 1985. 313-316. 1985
FULL JOURNAL NAME: Japanese Journal of Veterinary Science
CODEN: NJUZA
RECORD TYPE: Citation
LANGUAGE: ENGLISH
DESCRIPTORS: PATHOGENICITY DNA ELECTROPHORESIS
CONCEPT CODES:
  31000 Physiology and Biochemistry of Bacteria
  31500 Genetics of Bacteria and Viruses
  36002 Medical and Clinical Microbiology-Bacteriology
  10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
  10504 Biophysics-General Biophysical Techniques
BIOSYSTEMATIC CODES:
  04910 Bacteroidaceae (1979-)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA):
  Microorganisms
  Bacteria

11/9/18 (Item 18 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

03646210 BIOSIS NO.: 000074061787

PLASMID CONTENT OF SOME ORAL MICROORGANISMS ISOLATED FROM SUBGINGIVAL PLAQUE
AUTHOR: VANDENBERGH P A; SYED S A; GONZALEZ C F; LOESCHE W J; OLSEN R H
AUTHOR ADDRESS: MICROLIFE GENET., POB 2339, 1817-57TH ST., SARASOTA, FLA. 33578.
JOURNAL: J DENT RES 6 (3). 1982. 497-501. 1982
FULL JOURNAL NAME: Journal of Dental Research
CODEN: JDREA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Eight-five strains of bacterial species selected from the predominant cultivable dental plaque flora of patients with different periodontal pathologies were examined for their *plasmid* content. Actinomyces viscosus, A. odontolyticus, Bacteroides melaninogenicus ssp. asaccharolyticus, B. melaninogenicus ssp. intermedius, B. melaninogenicus ssp. melaninogenicus, B. ochraceus and *Fusobacterium* nucleatum were studied. Three B. melaninogenicus isolates showed *plasmids* of .apprx. 2.7-2.9 Mdalton molecular size. Restriction enzyme digests of the *plasmids* demonstrated dissimilar patterns when electrophoresed on agarose gels. In other bacteria, including Actinomyces ssp., *plasmids* were not observed.

DESCRIPTORS: HUMAN ACTINOMYCES-VISCOSUS ACTINOMYCES-ODONTOLYTICUS BACTEROIDES-MELANINOGENICUS-SSP-ASACCHAROLYTICUS BACTEROIDES-MELANINOGENICUS-SSP-INTERMEDIUS BACTEROIDES-MELANINOGENICUS-SSP-MELANINOGENICUS BACTEROIDES-OCHRACEUS *FUSOBACTERIUM*-NUCLEATUM MOLECULAR SIZE RESTRICTION ENZYME ELECTROPHORESIS
CONCEPT CODES:
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
10506 Biophysics-Molecular Properties and Macromolecules
19006 Dental and Oral Biology-Pathology
31000 Physiology and Biochemistry of Bacteria
36002 Medical and Clinical Microbiology-Bacteriology
10056 Biochemical Methods-Lipids
10064 Biochemical Studies-Proteins, Peptides and Amino Acids
10068 Biochemical Studies-Carbohydrates
10504 Biophysics-General Biophysical Techniques
10804 Enzymes-Methods
12100 Movement (1971-)
15002 Blood, Blood-Forming Organs and Body Fluids-Blood and Lymph Studies
19001 Dental and Oral Biology-General; Methods
31500 Genetics of Bacteria and Viruses
32000 Microbiological Apparatus, Methods and Media
BIOSYSTEMATIC CODES:
04910 Bacteroidaceae (1979-)
05810 Actinomycetaceae (1979-)
86215 Hominidae
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA):
Microorganisms
Bacteria
Animals
Chordates
Vertebrates
Mammals
Primates
Humans

11/9/19 (Item 19 from file: 5)

02826840 BIOSIS NO.: 000018059960
NOVEL *PLASMIDS* FROM ORAL BACTERIA ASSOCIATED WITH PERIODONTAL DISEASE
AUTHOR: VANDENBEGH P A; GONZALEZ C F; SYED S A; LOESCHE W J; OLSEN R H
AUTHOR ADDRESS: UNIV. MICH. MED. SCH., ANN ARBOR, MICH. 48109, USA.
JOURNAL: 80TH ANNUAL MEETING, MIAMI BEACH, FLA., USA, MAY 11-16, 1980. ABSTR ANNU MEET AM SOC MICROBIOL 80 (0). 1980. ABSTRACT 388. 1980
CODEN: ASMAC

DOCUMENT TYPE: Meeting
RECORD TYPE: Citation
LANGUAGE: ENGLISH
DESCRIPTORS: ABSTRACT HUMAN DENTAL PLAQUE ACTINOMYCES-SPP BACTEROIDES-SPP
FUSOBACTERIUM-NUCLEATUM DNA
CONCEPT CODES:
  10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
  10506 Biophysics-Molecular Properties and Macromolecules
  19006 Dental and Oral Biology-Pathology
  31000 Physiology and Biochemistry of Bacteria
  36002 Medical and Clinical Microbiology-Bacteriology
  00520 General Biology-Symposia, Transactions and Proceedings of
         Conferences, Congresses, Review Annuals
  10010 Comparative Biochemistry, General
  10052 Biochemical Methods-Nucleic Acids, Purines and Pyrimidines
  30500 Morphology and Cytology of Bacteria
  32000 Microbiological Apparatus, Methods and Media
BIOSYSTEMATIC CODES:
  04910 Bacteroidaceae (1979-)
  05810 Actinomycetaceae (1979-)
  86215 Hominidae
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA):
  Microorganisms
  Bacteria
  Animals
  Chordates
  Vertebrates
  Mammals
  Primates
  Humans

 11/9/20 (Item 1 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci

07921913 Genuine Article#: G2068 Number of References: 30
Title: INTERGENERIC PROTOPLAST FUSION BETWEEN *FUSOBACTERIUM*-VARIUM AND
   ENTEROCOCCUS-FAECIUM FOR ENHANCING DEHYDRODIVANILLIN DEGRADATION
Author(s): CHEN W; OHMIYA K; SHIMIZU S
Corporate Source: NAGOYA UNIV,SCH AGR,DEPT FOOD SCI & TECHNOL,CHIKUSA
   KU/NAGOYA/AICHI 464/JAPAN/
Journal: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1987, V53, N3, P542-548
Language: ENGLISH Document Type: ARTICLE
Geographic Location: JAPAN
Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences; CC AGRI--
   Current Contents, Agriculture, Biology & Environmental Sciences
Journal Subject Category: MICROBIOLOGY
Research Fronts: 86-1382 003 (HEMAGGLUTININ NEURAMINIDASE GENE OF
   NEWCASTLE-DISEASE VIRUS; NUCLEOTIDE-SEQUENCE ANALYSIS; TRANSCRIPTION OF
   GENES; CDNA CLONE)
  86-1657 001 (AMINOGLYCOSIDE PHOSPHOTRANSFERASE GENE; RECOMBINANT
   PLASMID VECTORS; EXPRESSION IN STREPTOMYCES-LIVIDANS; ANTIBIOTIC
   PRODUCING MICROORGANISMS)
Cited References:
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   CHEN W, 1985, V49, P211, APPL ENV MICROBIOL
   CHEN W, 1986, V52, P612, APPL ENV MICROBIOL
   FLEISCHER ER, 1985, V131, P919, J GEN MICROBIOL
   FODOR K, 1976, V73, P2147, P NATL ACAD SCI USA
   GASSON MJ, 1980, V9, P99, FEMS MICROBIOL LETT
   HEALY JB, 1980, V39, P436, APPL ENVIRON MICROB
   HOLDEMAN LV, 1977, P23, ANAEROBE LABORATORY
   HOPWOOD DA, 1981, V35, P237, ANNU REV MICROBIOL
   HOTCHKISS RD, 1980, V77, P3553, P NAT ACAD SCI US-B
   JONES DT, 1985, V131, P1213, J GEN MICROBIOL
   KANEKO H, 1979, V43, P1007, AGRIC BIOL CHEM
   LEWIS LA, 1969, V59, P359, J GEN MICROBIOL
   MANIATIS T, 1982, MOL CLONING LABORATO
   OCHI K, 1979, V139, P984, J BACTERIOL
   OH YK, 1980, V21, P219, DEV IND MICROBIOL

OKAMOTO T, 1983, V47, P2675, AGR BIOL CHEM TOKYO
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PEBERDY JF, 1980, V2, P23, ENZYME MICROB TECH
PETTEY TM, 1984, V47, P439, APPL ENV MICROBIOL
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SAITO H, 1963, V72, P619, BIOCHIM BIOPHYS ACTA
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SCHAEFFER P, 1976, V73, P2125, P NATL ACAD SCI US
SMITH MD, 1985, V162, P92, J BACTERIOL
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TAYA M, 1979, V57, P178, J FERMENT TECHNOL
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11/9/21 (Item 2 from file: 434)
DIALOG(R)File 434:SciSearch(R) Cited Ref Sci

07568945 Genuine Article#: E3054 Number of References: 27
Title: PROTOPLAST FORMATION AND REGENERATION OF DEHYDRODIVANILLIN-DEGRADING STRAINS OF *FUSOBACTERIUM*-VARIUM AND ENTEROCOCCUS-FAECIUM
Author(s): CHEN W; OHMIYA K; SHIMIZU S
Corporate Source: NAGOYA UNIV,SCH AGR,DEPT FOOD SCI & TECHNOL/NAGOYA/AICHI 464/JAPAN/
Journal: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, 1986, V52, N4, P612-616
Language: ENGLISH Document Type: ARTICLE
Geographic Location: JAPAN
Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences; CC AGRI--Current Contents, Agriculture, Biology & Environmental Sciences
Journal Subject Category: MICROBIOLOGY
Research Fronts: 86-1168 001 (ELECTROFUSION OF YEAST PROTOPLASTS; TOBACCO MOSAIC-VIRUS RNA; FUSION OF PLANT-PROTOPLASTS; ELECTRIC FIELD-MEDIATED CELL-FUSION; STABLE TRANSFORMATION)
86-1657 001 (AMINOGLYCOSIDE PHOSPHOTRANSFERASE GENE; RECOMBINANT *PLASMID* VECTORS; EXPRESSION IN STREPTOMYCES-LIVIDANS; ANTIBIOTIC PRODUCING MICROORGANISMS)
Cited References:
ALLCOCK ER, 1982, V43, P719, APPL ENV MICROBIOL
CHEN W, 1985, V49, P211, APPL ENV MICROBIOL
ELBS K, 1916, V93, P1, J PRAKT CHEMIE
FODOR K, 1976, V73, P2147, P NATL ACAD SCI USA
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KANEKO H, 1979, V43, P1007, AGR BIOL CHEM TOKYO
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OGATA S, 1984, V30, P305, J GEN APPL MICROBIOL
OH YK, 1980, V21, P219, DEV IND MICROBIOL
OHMIYA K, 1983, V61, P25, J FERMENT TECHNOL
OKAMOTO T, 1983, V47, P259, AGR BIOL CHEM TOKYO
OKANISHI M, 1974, V80, P389, J GEN MICROBIOL
PEBERDY JF, 1980, V2, P23, ENZYME MICROB TECH
PETTEY TM, 1984, V47, P439, APPL ENV MICROBIOL
PICATAGGIO SK, 1983, V17, P121, EUR J APPL
POWER JB, 1970, V275, P1016, NATURE
SMITH MD, 1985, V162, P92, J BACTERIOL
TANAKA N, 1984, V195, P378, MOL GEN GENET
TAYA M, 1983, V61, P197, J FERMENT TECHNOL
WEISS RL, 1976, V128, P668, J BACTERIOL

11/9/22 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10483664 20115567 PMID: 10648549
Native *plasmids* of *Fusobacterium* nucleatum: characterization and use in development of genetic systems.
Haake SK; Yoder SC; Attarian G; Podkaminer K
Divisions of Associated Clinical Sciences, UCLA School of Dentistry, Los Angeles, California 90095-1668, USA. shaake@dent.ucla.edu
Journal of bacteriology (UNITED STATES) Feb 2000, 182 (4) p1176-80, ISSN 0021-9193 Journal Code: HH3
Contract/Grant No.: DE12639, DE, NIDCR
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
Three native *plasmids* of *Fusobacterium* nucleatum were characterized, including DNA sequence analysis of one *plasmid*, pFN1. A shuttle *plasmid*, pHS17, capable of transforming Escherichia coli and F. nucleatum ATCC 10953 was constructed with pFN1. pHS17 was stably maintained in the F. nucleatum transformants, and differences in the transformation efficiencies suggested the presence of a restriction-modification system in F. nucleatum.
Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Descriptors: *Fusobacterium* nucleatum--genetics--GE; **Plasmids*--genetics--GE; *Transformation, Bacterial; Amino Acid Sequence; DNA, Bacterial--analysis--AN; Endodeoxyribonucleases--chemistry--CH; Escherichia coli--genetics--GE; *Fusobacterium* nucleatum--enzymology--EN; Molecular Sequence Data; Sequence Analysis, DNA
Molecular Sequence Databank No.: GENBANK/AF159249; GENBANK/AF219231
CAS Registry No.: 0 (DNA, Bacterial); 0 (Plasmids)
Enzyme No.: EC 2.7.7.- (DNA relaxase); EC 3.1.- (Endodeoxyribonucleases)
Record Date Created: 20000223

11/9/23 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09822318 98348445 PMID: 9683480
Dentilisin activity affects the organization of the outer sheath of Treponema denticola.
Ishihara K; Kuramitsu HK; Miura T; Okuda K
Department of Microbiology, Oral Health Science Center, Tokyo Dental College, 1-2-2 Masago, Mihama-ku, Chiba 261-8502, Japan. ishihara@tdc.ac.jp
Journal of bacteriology (UNITED STATES) Aug 1998, 180 (15) p3837-44, ISSN 0021-9193 Journal Code: HH3
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
Prolyl-phenylalanine-specific serine protease (dentilisin) is a major extracellular protease produced by Treponema denticola. The gene, prtP, coding for the protease was recently cloned and sequenced (K. Ishihara, T. Miura, H. K. Kuramitsu, and K. Okuda, Infect. Immun. 64:5178-5186, 1996). In order to determine the role of this protease in the physiology and virulence of T. denticola, a dentilisin-deficient mutant, K1, was constructed following electroporation with a prtP-inactivated DNA fragment. No chymotrypsin-like protease activity was detected in the dentilisin-deficient mutant. In addition, the high-molecular-mass oligomeric protein characteristic of the outer sheath of the organism decreased in the mutant. Furthermore, the hydrophobicity of the mutant was decreased, and coaggregation of the mutant with *Fusobacterium* nucleatum was enhanced compared to that of the wild-type organism. The results obtained with a mouse abscess model system indicated that the virulence of the mutant was attenuated relative to that of the wild-type organism. These results suggest that dentilisin activity plays a major role in the structural organization of the outer sheath of T. denticola. The loss of dentilsin activity and the structural change in the outer sheath affect the pathogenicity of T. denticola.
Tags: Animal; Support, Non-U.S. Gov't
Descriptors: *Cell Membrane--ultrastructure--UL; *Chymotrypsin--metabolism--ME; *Treponema--physiology--PH; Cell Membrane--physiology--PH; Chymotrypsin--genetics--GE; Chymotrypsin--isolation and purification--IP

; Cloning, Molecular; Electrophoresis, Polyacrylamide Gel; Escherichia coli --genetics--GE; *Fusobacterium*--genetics--GE; Immunoblotting; Mice; Periodontal Abscess--microbiology--MI; Periodontal Abscess--physiopatholog y--PP; *Plasmids*; Polymerase Chain Reaction; Porphyromonas gingivalis --genetics--GE; Recombinant Proteins--biosynthesis--BI; Recombinant Proteins--isolation and purification--IP; Recombinant Proteins--metabolism --ME; Treponema--enzymology--EN; Treponema--genetics--GE; Treponema --pathogenicity--PY; Treponemal Infections--physiopathology--PP; Virulence
CAS Registry No.: 0 (Plasmids); 0 (Recombinant Proteins)
Enzyme No.: EC 3.4.21.- (dentilisin); EC 3.4.21.1 (Chymotrypsin)
Record Date Created: 19980820

11/9/24 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08154512 94204589 PMID: 8153579
Similarities between *Fusobacterium* nucleatum and bacteroides fragilis studied by two DNA probes derived from *Fusobacterium* nucleatum.
Bolstad AI; Kleivdal H; Jensen HB
Department of Biochemistry and Molecular Biology, University of Bergen, Norway.
Scandinavian journal of dental research (DENMARK) Feb 1994, 102 (1) p5-9, ISSN 0029-845X Journal Code: UCQ
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: DENTAL; INDEX MEDICUS
A polymerase chain reaction (PCR)-amplified oligonucleotide DNA probe corresponding to a *Fusobacterium* nucleatum FevI DNA region coding for a 40-kDa major outer-membrane protein (OMP) and a randomly cloned 2.1 kb DNA probe were found to recognize DNA from the Gram-negative bacteria *Fusobacterium* nucleatum and Bacteroides fragilis on Southern blots and slot blots. The results indicate sequence similarity within the DNA fragments studied. Immunoblots tested with polyclonal antibodies against whole cells of F. nucleatum revealed only weak antigen similarity between these species.
Tags: Comparative Study; Support, Non-U.S. Gov't
Descriptors: Bacteroides fragilis--classification--CL; *DNA Probes; * *Fusobacterium* nucleatum--classification--CL; Actinobacillus actinomycetem comitans--genetics--GE; Actinobacillus actinomycetemcomitans--immunology --IM; Bacterial Outer Membrane Proteins--analysis--AN; Bacteroides fragilis --genetics--GE; Bacteroides fragilis--immunology--IM; Blotting, Southern; Electrophoresis, Agar Gel; Electrophoresis, Polyacrylamide Gel; *Fusobacterium* nucleatum--genetics--GE; *Fusobacterium* nucleatum --immunology--IM; Immunoblotting; Oligonucleotide Probes; *Plasmids* --genetics--GE; Polymerase Chain Reaction
CAS Registry No.: 0 (Bacterial Outer Membrane Proteins); 0 (DNA Probes); 0 (Oligonucleotide Probes); 0 (Plasmids)
Record Date Created: 19940509

11/9/25 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07220020 90225757 PMID: 2327774
Genetic basis of tetracycline resistance in urogenital bacteria.
Roberts MC; Hillier SL
Department of Pathobiology, University of Washington, Seattle 98195.
Antimicrobial agents and chemotherapy (UNITED STATES) Feb 1990, 34 (2) p261-4, ISSN 0066-4804 Journal Code: 6HK
Contract/Grant No.: AI24136, AI, NIAID
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
The distributions of the nucleotide sequences related to the tetracycline resistance determinants Tet K, Tet L, Tet M, and Tet O were studied by dot blot hybridization with randomly chosen clinical urogenital tract isolates of viridans group streptococci, Streptococcus agalactiae, Enterococcus faecalis, Gardnerella vaginalis, Lactobacillus spp., *Fusobacterium*

nucleatum, Peptostreptococcus spp., and Veillonella parvula. Among the Peptostreptococcus spp., 79% of the isolates hybridized with one (64%) or more (36%) of the probes for Tet K (27%), Tet L (30%), Tet M (75%) and Tet O (13%). Of the viridans group streptococci, 82% of the strains hybridized with one (34%) or more (66%) of the four probes. The distribution of the four determinants in this group was as follows: Tet K, 36%; Tet L, 31%; Tet M, 43%; Tet O, 61%. Twenty-nine percent of the enterococci and forty-six percent of the group B streptococci hybridized with the probes; however, the Tet K, Tet L, and Tet O determinants were found in only a few strains, while the Tet M determinant predominated. A total of 29% of the F. nucleatum isolates, 55% of the G. vaginalis isolates, and 26% of the V. parvula isolates hybridized with the Tet M determinant. In contrast, 43% of the Lactobacillus spp. hybridized with the Tet O determinant. The data indicate that tetracycline resistance determinants are common to many of the microorganisms isolated from the urogenital tract.

Tags: Human; Support, U.S. Gov't, P.H.S.

Descriptors: *Bacteria--genetics--GE; *Tetracycline Resistance--genetics --GE; *Urogenital System--microbiology--MI; Bacteria--drug effects--DE; DNA Probes; DNA, Bacterial--analysis--AN; Nucleic Acid Hybridization; Peptostreptococcus--drug effects--DE; Peptostreptococcus--genetics--GE; *Plasmids*; Restriction Mapping

CAS Registry No.: 0 (DNA Probes); 0 (DNA, Bacterial); 0 (Plasmids)

Record Date Created: 19900516

11/9/26 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05929827 89252894 PMID: 3074019

Cloning the FnuDI, NaeI, NcoI and XbaI restriction-modification systems.

Van Cott EM; Wilson GG

New England Biolabs, Inc., Beverly, MA 01915.

Gene (NETHERLANDS) Dec 25 1988, 74 (1) p55-9, ISSN 0378-1119 Journal Code: FOP

Languages: ENGLISH

Document type: Journal Article

Record type: Completed

Subfile: INDEX MEDICUS

Methyltransferase genes from the FnuDI, NaeI, NcoI, and XbaI restriction-modification systems have been isolated in Escherichia coli by 'shot-gun' cloning bacterial DNA fragments into *plasmid* vectors and selecting for protectively modified molecules that resist digestion by the corresponding restriction endonuclease.

Descriptors: Deoxyribonucleases, Type II Site-Specific--genetics--GE; * *Fusobacterium*--genetics--GE; *Genes, Bacterial; *Nocardia--genetics--GE; *Site-Specific DNA Methyltransferase (Cytosine-Specific)--genetics--GE; *Site-Specific DNA-Methyltransferase (Adenine-Specific)--genetics--GE; *Xanthomonas--genetics--GE; Cloning, Molecular; Escherichia coli--genetics --GE; *Fusobacterium*--enzymology--EN; Genes, Structural; Nocardia --enzymology--EN; Recombinant Proteins--genetics--GE; Xanthomonas --enzymology--EN

CAS Registry No.: 0 (Recombinant Proteins)

Enzyme No.: EC 2.1.1.- (DNA modification methylase BspI); EC 2.1.1.- (DNA modification methylase NaeI); EC 2.1.1.- (DNA modification methylase NcoI); EC 2.1.1.- (DNA modification methylase XbaI); EC 2.1.1.72 (Site-Specific DNA-Methyltransferase (Adenine-Specific)); EC 2.1.1.73 (Site-Specific DNA Methyltransferase (Cytosine-Specific)); EC 3.1.21.- (endodeoxyribonuclease HaeIII); EC 3.1.21.- (endodeoxyribonuclease XBAI) ; EC 3.1.21.4 (Deoxyribonucleases, Type II Site-Specific)

Record Date Created: 19890626

11/9/27 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05427563 90075642 PMID: 2686914

Mechanisms of resistance in anaerobes and new developments in testing.

Finegold SM

Research Service, Wadsworth VA Medical Center, Los Angeles, CA 90073.

Diagnostic microbiology and infectious disease (UNITED STATES) Jul-Aug 1989, 12 (4 Suppl) p117S-120S, ISSN 0732-8893 Journal Code: DMI

Languages: ENGLISH
Document type: Journal Article; Review; Review, Tutorial
Record type: Completed
Subfile: INDEX MEDICUS

Anaerobic bacteria currently demonstrate increased resistance to antimicrobial agents, primarily by the production of beta-lactamase. A number of species of Bacteroides, most notably those in the Bacteroides fragilis group, produce these enzymes. A few species of *Fusobacterium* and Clostridium produce beta-lactamase as well. Fortunately, this mechanism of resistance is readily overcome by administering beta-lactamase inhibitors coupled with a beta-lactam antibiotic that would otherwise be inactivated. Other types of resistance encountered in anaerobic bacteria include inactivating enzymes such as chloramphenicol acetyltransferase, *plasmid* -mediated transferable multiple-drug resistance, changes in porin molecules in the outer membrane of the bacterial cell, decreased uptake of drug by other mechanisms, changes in the target organs such as penicillin-binding proteins, and decreased reduction of the antibiotic to an active intermediate product. In many institutions, certain drugs such as cefoxitin, clindamycin, and piperacillin, which were previously active against almost all strains of B. fragilis, are now effective against only 70 to 85% of this group of anaerobes. Drugs with essentially 100% activity against most anaerobic bacteria include chloramphenicol, imipenem, metronidazole, and the combinations of a beta-lactam antibiotic plus a beta-lactamase inhibitor such as ampicillin plus sulbactam and amoxicillin or ticarcillin combined with sodium clavulanate. This paper also discusses the indications for antimicrobial susceptibility testing of anaerobes as well as problems encountered with testing techniques that are currently being used. (28 Refs.)

Tags: Human

Descriptors: *Bacteria, Anaerobic--drug effects--DE; *Drug Resistance, Microbial; *Microbial Sensitivity Tests; Bacteria, Anaerobic--genetics--GE; Bacterial Infections--drug therapy--DT; Bacteroides--drug effects--DE; Bacteroides--genetics--GE; Drug Resistance, Microbial--genetics--GE; Drug Resistance, Microbial--physiology--PH

Record Date Created: 19900117

11/9/28 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03767880 83119256 PMID: 6760336

Antibiotic resistance in anaerobic bacteria: molecular biology and clinical aspects.

Bawdon RE; Crane LR; Palchaudhuri S

Reviews of infectious diseases (UNITED STATES) Nov-Dec 1982, 4 (6) p1075-95, ISSN 0162-0886 Journal Code: SXN

Languages: ENGLISH
Document type: Journal Article; Review
Record type: Completed
Subfile: INDEX MEDICUS

The patterns of antibiotic susceptibility among anaerobes isolated in the United States during the past 14 years were reviewed. Resistance to the tetracyclines, the penicillins, clindamycin, and other antibiotics has emerged among strains of Bacteroides, Clostridium, and anaerobic cocci. Genetic transfer of antibiotic resistance has been documented in anaerobic environments. Inter- and intrageneric transfer by conjugation and transformation has been described. *Plasmids* have been identified in anaerobes, and conjugal transfer of antibiotic resistance has been reported. The biochemical mechanisms of antibiotic resistance in anaerobes are similar to those described for aerobes. There are some differences in drug transport and inhibitory actions. Antibiotic resistant anaerobes have been isolated from patients participating in large comparative studies of anaerobic infections involving abdominal, pelvic, and pleuropulmonary sites, but instances in which treatment has failed as a result of resistance have not been found. Reports describing small numbers of patients or individual cases have documented the failure of therapy in clinical and laboratory infections caused by both sensitive or resistant anaerobic bacteria. Patterns of antibiotic susceptibility among clinically important anaerobes need to be monitored periodically in several geographic regions. (159 Refs.)

Tags: Animal; Human; Support, Non-U.S. Gov't

Descriptors: *Gram-Negative Anaerobic Bacteria--growth and development --GD; *Peptostreptococcus--growth and development--GD; Abdomen; Abscess --drug therapy--DT; Bacteroides--enzymology--EN; Bacteroides--genetics--GE ; Bacteroides--growth and development--GD; Bacteroides Infections--drug therapy--DT; Carbenicillin--pharmacology--PD; Cephalosporins--pharmacology --PD; Clindamycin--pharmacology--PD; Clostridium--enzymology--EN; Clostrid ium--growth and development--GD; *Fusobacterium*--growth and development --GD; Genes, Bacterial--drug effects--DE; Mice; Nitroimidazoles --pharmacology--PD; Penicillin G--pharmacology--PD; Penicillin Resistance; *Plasmids*--drug effects--DE; Pleuropneumonia--drug therapy--DT; Rats; Tetracycline--pharmacology--PD; beta-Lactamases--metabolism--ME

CAS Registry No.: 0 (Cephalosporins); 0 (Nitroimidazoles); 0 (Plasmids); 18323-44-9 (Clindamycin); 4697-36-3 (Carbenicillin); 60-54-8 (Tetracycline); 61-33-6 (Penicillin G)

Enzyme No.: EC 3.5.2.6 (beta-Lactamases)

Record Date Created: 19830311

```
?s fusobacterium and shuttle
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          12801  SHUTTLE
     S12       5  FUSOBACTERIUM AND SHUTTLE
?rd
...completed examining records
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?s s13 and coli
              4  S13
         504931  COLI
     S14       4  S13 AND COLI
?t/9/all

 14/9/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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```

12360222 BIOSIS NO.: 200000113724

Native plasmids of *Fusobacterium* nucleatum: Characterization and use in development of genetic systems.

AUTHOR: Kinder Haake Susan(a); Yoder Sean C; Attarian Gwynne; Podkaminer Kara

AUTHOR ADDRESS: (a)Section of Periodontics, UCLA School of Dentistry, 10833 Le Conte Ave., Los Angeles, CA, 90095-1668**USA

JOURNAL: Journal of Bacteriology 182 (4):p1176-1180 Feb., 2000

ISSN: 0021-9193

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT: Three native plasmids of *Fusobacterium* nucleatum were characterized, including DNA sequence analysis of one plasmid, pFN1. A *shuttle* plasmid, pHS17, capable of transforming Escherichia *coli* and F. nucleatum ATCC 10953 was constructed with pFN1. pHS17 was stably maintained in the F. nucleatum transformants, and differences in the transformation efficiencies suggested the presence of a restriction-modification system in F. nucleatum.

DESCRIPTORS:

MAJOR CONCEPTS: Molecular Genetics (Biochemistry and Molecular Biophysics)

BIOSYSTEMATIC NAMES: Bacteroidaceae--Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Enterobacteriaceae--Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms

ORGANISMS: Escherichia *coli* (Enterobacteriaceae); *Fusobacterium* nucleatum (Bacteroidaceae)--strain-ATCC 10953

BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Microorganisms

CHEMICALS & BIOCHEMICALS: pFN1--*Fusobacterium* nucleatum native plasmid, characterization, *shuttle* plasmid; pFN1. pHS17

METHODS & EQUIPMENT: DNA sequence analysis--analytical method, molecular genetic method

MISCELLANEOUS TERMS: restriction-modification system

CONCEPT CODES:

31500 Genetics of Bacteria and Viruses
10052 Biochemical Methods-Nucleic Acids, Purines and Pyrimidines
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
32000 Microbiological Apparatus, Methods and Media
10506 Biophysics-Molecular Properties and Macromolecules
31000 Physiology and Biochemistry of Bacteria
BIOSYSTEMATIC CODES:
06702 Enterobacteriaceae (1992-)
06901 Bacteroidaceae (1992-)

14/9/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12030651 BIOSIS NO.: 199900311170
Transformation of *Fusobacterium* nucleatum by electroporation.
AUTHOR: Haake S Kinder(a); Yoder S C(a)
AUTHOR ADDRESS: (a)School of Dentistry, UCLA, Los Angeles, CA**USA
JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 99p331 1999
CONFERENCE/MEETING: 99th General Meeting of the American Society for Microbiology Chicago, Illinois, USA May 30-June 3, 1999
SPONSOR: American Society for Microbiology
ISSN: 1060-2011
RECORD TYPE: Citation
LANGUAGE: English
DESCRIPTORS:
MAJOR CONCEPTS: Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
BIOSYSTEMATIC NAMES: Bacteroidaceae--Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms; Enterobacteriaceae--Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms
ORGANISMS: E. *coli* {Escherichia *coli*} (Enterobacteriaceae); *Fusobacterium* nucleatum (Bacteroidaceae)
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): Bacteria; Eubacteria; Microorganisms
CHEMICALS & BIOCHEMICALS: pHS17--*shuttle* plasmid; DNA--transfer
METHODS & EQUIPMENT: electroporation--DNA transfer method
MISCELLANEOUS TERMS: Meeting Abstract; Meeting Poster
CONCEPT CODES:
31500 Genetics of Bacteria and Viruses
10050 Biochemical Methods-General
10060 Biochemical Studies-General
32000 Microbiological Apparatus, Methods and Media
31000 Physiology and Biochemistry of Bacteria
00520 General Biology-Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals
BIOSYSTEMATIC CODES:
06702 Enterobacteriaceae (1992-)
06901 Bacteroidaceae (1992-)

14/9/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09974676 BIOSIS NO.: 199598429594
Insertional inactivation of binding determinants of Streptococcus crista CC5A using Tn916.
AUTHOR: Correia F F; Dirienzo J M; Lamont R J; Anderman C; McKay T L; Rosan Burton(a)
AUTHOR ADDRESS: (a)Dep. Microbiol., Sch. Dent. Med., Univ. Pa., 4001 Spruce St., Philadelphia, PA 19104-6002**USA
JOURNAL: Oral Microbiology and Immunology 10 (4):p220-226 1995
ISSN: 0902-0055
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Intermicrobial binding plays an important role in the ecology of

the oral cavity because it represents one mechanism by which specific bacteria colonize dental plaque. The formation of "corncobs", a morphologically distinct microbial unit composed of Streptococcus crista and *Fusobacterium* nucleatum, is a highly specific binding interaction that depends on the presence of polar tufts of fimbriae on the streptococci. We have used a genetic approach to examine the role of streptococcal cell surface components involved in the binding of S. crista to F. nucleatum. Such binding may be an important component of corncob formation. A method for the genetic transformation of S. crista was used to transfer the broad host range transposon, Tn916, into the bacteria. Cells were grown to early log phase in brain heart infusion broth containing 10% fetal calf serum. The competent cells were mixed with purified DNA from pDL916, a plasmid construct consisting of Tn916 and the streptococcal/Escherichia *coli* *shuttle* vector pDL278. Over 300 transformants were screened for a reduction in binding to F. nucleatum. Five of the transformants showed a change in binding ranging from 59% to 29% of the positive control values. Southern blots revealed that the binding-deficient transformants contained the Tn916 element integrated into one of 4 different sites in the chromosome. The transposon, integrated into 4 different sites, appeared to be stable in the absence of selective pressure. Based on these findings, it appears that some strains of S. crista are naturally competent and that insertional inactivation methods can be used to facilitate the study of binding receptors in this group of oral streptococci.

DESCRIPTORS:
MAJOR CONCEPTS: Biochemistry and Molecular Biophysics; Genetics; Membranes (Cell Biology); Physiology
BIOSYSTEMATIC NAMES: Bacteroidaceae--Eubacteria, Bacteria; Gram-Positive Cocci--Eubacteria, Bacteria
ORGANISMS: gram-positive cocci (Gram-Positive Cocci); *Fusobacterium* nucleatum (Bacteroidaceae); Streptococcus crista (Gram-Positive Cocci
BIOSYSTEMATIC CLASSIFICATION (SUPER TAXA): bacteria; eubacteria; microorganisms
MISCELLANEOUS TERMS: BINDING RECEPTOR; CELL SURFACE COMPONENT; DNA TRANSFER
CONCEPT CODES:
10506 Biophysics-Molecular Properties and Macromolecules
10508 Biophysics-Membrane Phenomena
31000 Physiology and Biochemistry of Bacteria
31500 Genetics of Bacteria and Viruses
10062 Biochemical Studies-Nucleic Acids, Purines and Pyrimidines
BIOSYSTEMATIC CODES:
06901 Bacteroidaceae (1992-)
07700 Gram-Positive Cocci (1992-)

14/9/4 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10483664 20115567 PMID: 10648549
Native plasmids of *Fusobacterium* nucleatum: characterization and use in development of genetic systems.
Haake SK; Yoder SC; Attarian G; Podkaminer K
Divisions of Associated Clinical Sciences, UCLA School of Dentistry, Los Angeles, California 90095-1668, USA. shaake@dent.ucla.edu
Journal of bacteriology (UNITED STATES) Feb 2000, 182 (4) p1176-80, ISSN 0021-9193 Journal Code: HH3
Contract/Grant No.: DE12639, DE, NIDCR
Languages: ENGLISH
Document type: Journal Article
Record type: Completed
Subfile: INDEX MEDICUS
Three native plasmids of *Fusobacterium* nucleatum were characterized, including DNA sequence analysis of one plasmid, pFN1. A *shuttle* plasmid, pHS17, capable of transforming Escherichia *coli* and F. nucleatum ATCC 10953 was constructed with pFN1. pHS17 was stably maintained in the F. nucleatum transformants, and differences in the transformation efficiencies suggested the presence of a restriction-modification system in F. nucleatum.
Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.

Descriptors: *Fusobacterium* nucleatum--genetics--GE; *Plasmids--genetics --GE; *Transformation, Bacterial; Amino Acid Sequence; DNA, Bacterial --analysis--AN; Endodeoxyribonucleases--chemistry--CH; Escherichia *coli* --genetics--GE; *Fusobacterium* nucleatum--enzymology--EN; Molecular Sequence Data; Sequence Analysis, DNA

Molecular Sequence Databank No.: GENBANK/AF159249; GENBANK/AF219231

CAS Registry No.: 0 (DNA, Bacterial); 0 (Plasmids)

Enzyme No.: EC 2.7.7.- (DNA relaxase); EC 3.1.- (Endodeoxyribonucleases)

Record Date Created: 20000223

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24aug01 17:40:18 User259980 Session D148.2

$6.78 1.210 DialUnits File5

$41.25 25 Type(s) in Format 9

$41.25 25 Types

$48.03 Estimated cost File5

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$8.40 2 Type(s) in Format 9

$8.40 2 Types

$12.36 Estimated cost File434

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$1.80 9 Type(s) in Format 9

$1.80 9 Types

$5.65 Estimated cost File155

OneSearch, 3 files, 2.690 DialUnits FileOS

$0.35 TYMNET

$66.39 Estimated cost this search

$66.64 Estimated total session cost 2.762 DialUnits

Status: Signed Off. (7 minutes)

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### Status: Path 1 of [Dialog Information Services via Modem]

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Trying 3106900061...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ******** HHHHHHHH SSSSSSSS?
### Status: Signing onto Dialog
 ********
ENTER PASSWORD:
 ******** HHHHHHHH SSSSSSSS? ********
Welcome to DIALOG
### Status: Connected


Dialog level 01.08.22D

Last logoff:  24aug01 17:40:18
Logon file001 27aug01 11:18:42
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                    ***
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                    ***
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***IBISWorld Market Research (File 753)
***Investext PDF Index (File 745)
***Daily and Sunday Telegraph (London) Papers (File 756)
***The Mirror Group Publications (United Kingdom) (File 757)

UPDATING RESUMED
***Delphes European Business (File 481)
***Books In Print (File 470)
                             ***
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***Kompass Asia/Pacific (File 592)
***Kompass Central/Eastern Europe (File 593)
***Kompass Canada (File 594)
***CANCERLIT (File 159)
***Information Science Abstracts (File 202)

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 * * *                                    * * *

File   1:ERIC  1966-2001/Aug 17
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        (c) 1998 Inst for Sci Info
  File   5:Biosis Previews(R)  1969-2001/Aug W3
        (c) 2001 BIOSIS
  File 155:MEDLINE(R)  1966-2001/Sep W3

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E6         2  AU=KINDER I
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E8       186  AU=KINDER J E
E9         1  AU=KINDER J M
E10        1  AU=KINDER J P
E11        3  AU=KINDER J W
E12        3  AU=KINDER JAMES E

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 1/3/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09133878   97180042   PMID: 9028259
 Effect  of  oral bacteria on peripheral blood leukocyte interleukin-6 and
soluble interleukin-6 receptor production.
  Lindemann RA; *Kinder Haake SA*; Kjeldsen M; Avanessian AB
  Section of Oral Biology, UCLA School of Dentistry 90095-1668, USA.
  Oral microbiology and immunology (DENMARK)   Oct 1996,  11  (5)  p332-6,
ISSN 0902-0055   Journal Code: ORA
  Contract/Grant No.: CA-16042, CA, NCI; DE09174, DE, NIDCR
  Languages: ENGLISH
  Document type: Journal Article
  Record type: Completed
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E3         0 *AU=FINEGOLD, SM
E4         1  AU=FINEGOLDS M
E5        19  AU=FINEGOOD D
E6        69  AU=FINEGOOD D T
E7         5  AU=FINEGOOD DIANE
E8        36  AU=FINEGOOD DIANE T
E9        85  AU=FINEGOOD DT
E10        6  AU=FINEK J
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E12        1  AU=FINEKLSHTEIN SK

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E19        6  AU=FINELEVY JB
E20        1  AU=FINELHOR DAVID
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E22        7  AU=FINELL B
E23        3  AU=FINELL G
E24        3  AU=FINELL GR

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              13  PFN1
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      S3       2  RD (unique items)
?t/3/all

 3/3/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
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12360222   BIOSIS NO.: 200000113724
Native plasmids of *Fusobacterium* nucleatum: Characterization and use in
 development of genetic systems.
AUTHOR: Kinder Haake Susan(a); Yoder Sean C; Attarian Gwynne; Podkaminer
  Kara
AUTHOR ADDRESS: (a)Section of Periodontics, UCLA School of Dentistry, 10833
  Le Conte Ave., Los Angeles, CA, 90095-1668**USA
JOURNAL: Journal of Bacteriology  182 (4):p1176-1180 Feb., 2000
ISSN: 0021-9193
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English


 3/3/2     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10483664   20115567   PMID: 10648549
 Native plasmids of *Fusobacterium* nucleatum: characterization and use in
development of genetic systems.
  Haake SK; Yoder SC; Attarian G; Podkaminer K
  Divisions  of Associated Clinical Sciences, UCLA School of Dentistry, Los
Angeles, California 90095-1668, USA. shaake@dent.ucla.edu
  Journal of bacteriology (UNITED STATES)   Feb 2000,  182  (4)  p1176-80,
ISSN 0021-9193   Journal Code: HH3
  Contract/Grant No.: DE12639, DE, NIDCR
  Languages: ENGLISH
  Document type: Journal Article
  Record type: Completed
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               $1.65  1 Type(s) in Format  3
            $1.65  1 Types
     $3.06  Estimated cost File5
            $1.01    0.314 DialUnits File155
               $0.40  2 Type(s) in Format  3
            $0.40  2 Types
     $1.41  Estimated cost File155
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OneSearch, 3 files, 0.650 DialUnits FileOS
$0.20 TYMNET
$5.87 Estimated cost this search
$6.43 Estimated total session cost 0.796 DialUnits

Status: Signed Off. (5 minutes)